

SEQUENCE LISTING

<110> Bejanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US2.REG

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<141> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 112

<170> JPatent

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cgttgccaca	gtttttgatga	tcatctctct	cccaaccaag	atggtggaaa	aagcaaaaac	180
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tgtgagccag	ggacaattcc	tgatgcctcc	atcctagcag	ctgccttgga	tctactatgc	300
ggcattcttc	tgattcattt	ttctccattt	gtgctgtttt	tctctgtgat	gtgaatccat	360
ccctatccat	tatgtcatgc	ctccatcttt	tgctgcttct	tcagattgca	ctgagccata	420
agaggaagcc	cctgtggtgg	ccagagcagc	cttggttctg	gaatgtgctc	gttttgttca	480
ccgctgcaac	cgtggcaact	ggccagagtg	gatgaaaggg	caccacgtga	acatcaccaa	540
gaaaggactt	tcccggggac	gctctcccat	tgtgggcaac	aagcgaaacc	agaagctgca	600

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taaagagggtt ccatatattc ctcttttctt aaagattact tggaataact gttacaattt 780
ccgttaataa ttcagctgaa tgtgtctacc aatgtgctta ccaactaagg caattggcgt 840
ccgattgaat gagctgtgcc acggggaaaag tgagagccca gccaacctgc tgggtctcat 900
ttacgatgaa gagaccaaga ggagacttag aaaggaggat gaggaggaag actttttaga 960
tgacattcca ctttcaagtc aatacacagc tcattcttgca tttaaaagct gattatggtg 1020
caagcaactt tcgggctgga aattctacag aagcttgtct tttccattct tgatgagagg 1080
caaagtcccc ggcaacaaat taactcagga gagaaaatgg ttttcctgaa aaaaacgata 1140
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gtctaaatct gattgaatag cagcgtagaa atcttgcgaa attacttccc atttctgttt 1380
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Met
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gca gca tgt cag ctt ctt ctg gag att acc acc ttc ctg cga gag acc 1485
Ala Ala Cys Gln Leu Leu Leu Glu Ile Thr Thr Phe Leu Arg Glu Thr
5 10 15
ttt tct tgc ctg ccc aga cct cgc act gag cct ctg gtg gct tca acg 1533
Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
20 25 30
gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg 1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
35 40 45
atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag 1629
Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
50 55 60 65
gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa 1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
70 75 80
aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac 1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
85 90 95
cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att 1773
Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
100 105 110
gcg ggc ctc acc att gca tgc aat gac tat ttt gta gta cac atg aag 1821
Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
115 120 125
cag aag gga aag aag taggcagaaa tgagcagttc gctcctccct gataagagtt 1876
Gln Lys Gly Lys Lys
130
gtcccaaagg gtcgcttaag gaatctgccc cacagcttcc cccatagaag gatttcatga 1936
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Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr
35 40 45
Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr
50 55 60
Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu
65 70 75 80

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Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu
 85 90 95
 Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu
 100 105 110
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 Lys Gln Lys Gly Lys Lys
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<220>
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 Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Pro Leu Leu Gly
 -15 -10 -5
 ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa 152
 Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
 1 5 10
 gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg 200
 Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp
 15 20 25
 ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg 248
 Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu
 30 35 40 45
 gtc atg tgg ctt cag ggc ggt cca ggc ggt tct agc act gga ttt gga 296
 Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly
 50 55 60
 aac ttt gag gaa att ggg ccc ctt gac agt gat ctc aaa cca cgg aaa 344
 Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys
 65 70 75
 acc acc tgg ctc cag gct gcc agt ctc cta ttt gtg gat aat ccc gtg 392
 Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val
 80 85 90
 ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac 440
 Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp
 95 100 105
 ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc 488

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Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
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agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag 536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu
          130          135          140
tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag 584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys
          145          150          155
gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg 632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu
          160          165          170
ggg gat tcc tgg atc tcc cct gtt gat tgc gtc ctc tcc tgg gga cct 680
Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro
          175          180          185
tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg 728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val
          190          195          200          205
tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac 776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr
          210          215          220
aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag 824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln
          225          230          235
gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt 872
Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly
          240          245          250
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac 917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His
          255          260          265
tgaggctccc cacatatctg caaatgattg catgctggat aataaatctc ttgggtctaa 977
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 <213> Homo sapiens

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-10          -5          1          5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
          10          15          20
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
          25          30          35
Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
          40          45          50
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
          55          60          65          70
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu
          75          80          85
Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser
          90          95          100
Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val
          105          110          115
Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro
          120          125          130

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Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile
 135 140 145 150
 Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn
 155 160 165
 Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser
 170 175 180
 Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp
 185 190 195
 Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 200 205 210
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala
 215 220 225 230
 Glu Met Ile Ile Glu Gln Val Lys Arg Gly Asn Thr Gln Arg Leu Ala
 235 240 245
 Cys Leu Ala Phe Ser Gly Gly Tyr Arg Ala His Gly Trp Cys Cys Gln
 250 255 260
 Thr Trp Ser Leu His
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<220>
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 <222> 423..438

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 Met Lys Phe Phe Val Phe Ala Leu Val Leu
 -15 -10
 gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161
 Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His
 -5 1 5
 cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209
 His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
 10 15 20
 aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257
 Thr Leu Leu Pro Leu Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
 25 30 35 40
 aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
 Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
 45 50 55
 tca att gtc act tgatgatata attgcaatth aaactgttaa gctgtgttca 357
 Ser Ile Val Thr

gtactgtttc tgaataatag aaatcacttc tctaaaagca ataaatttca agcacatttt 417
 taaataaaaa aaaaaaaaaa a 438

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 <222> 1..19

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 1 5 10
 Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
 15 20 25
 Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
 30 35 40 45
 Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
 50 55

<210> 7
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 Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
 -10 -5 1
 atg act cag tct cca ctc ttc ctg ccc gtc acc cct gga gag ccg gcc 148
 Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala
 5 10 15 20
 tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc 196
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Val Gln Gly Ser
 25 30 35

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aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc 244
Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
40 45 50
ctg ata tac ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 292
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
55 60 65
agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg 340
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
70 75 80
gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act 388
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
85 90 95 100
cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg 436
Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
105 110 115
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 484
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
120 125 130
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 532
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
135 140 145
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 580
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
150 155 160
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 628
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165 170 175 180
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 676
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
185 190 195
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 724
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
200 205 210
aag agc ttc aac agg gga gag tgt tagagggaga agtgcccca cctgctctc 778
Lys Ser Phe Asn Arg Gly Glu Cys
215 220
agttccagcc tgacccctc ccatcctttg gcctctgacc ctttttccac aggggaccta 838
cccctattgc ggtcctccag ctcatctttc acctcaccoc cctcctcctc cttggcttta 898
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 1 5 10
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 15 20 25
 Leu Leu His Val Gln Gly Ser Asn Tyr Leu Asp Trp Tyr His Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75

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Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      80      85      90
Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg
      95      100      105
Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
      110      115      120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
      125      130      135      140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
      145      150      155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
      160      165      170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
      175      180      185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
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Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
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gattaatcca tggcaggcc tggaaaagtt ccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccct 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
      Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
      -10      -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
      1      5      10      15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
      20      25      30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65      70      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634

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ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcaggtg 694
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Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
20 25 30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35 40 45 50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
55 60 65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
70 75 80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
85 90

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gattaatcca tgggcaggcc tggaaaagt cccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccct 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
-10 -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
1 5 10 15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
20 25 30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
35 40 45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481

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Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
   50                               55                               60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
   65                               70                               75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
   80                               85                               90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<210> 12
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
   5          10          15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
  20          25          30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35          40          45          50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
          55          60          65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
  70          75          80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
   85          90

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<210> 13
 <211> 732
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..732

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<400> 13
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tcttcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgt 120
gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
          Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
          -10          -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337

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Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1      5      10
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
      20      25      30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65      70      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt attatccaca ttttgagat gaggaacag agtcaggatga 694
agtgtctttt ccaaggccaa gctcctgagg gcaggggc 732

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<210> 14
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 <212> PRT
 <213> Homo sapiens

<220>
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 <222> 1..14

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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
      5      10      15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20      25      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35      40      45      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55      60      65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
      70      75      80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      85      90

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<210> 15
 <211> 733
 <212> DNA
 <213> Homo sapiens

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 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..733

<400> 15

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 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289

Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala

-10

-5

aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly

1

5

10

15

atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys

20

25

30

ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys

35

40

45

tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser

50

55

60

ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu

65

70

75

agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser

80

85

90

tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<211> 107

<212> PRT

<213> Homo sapiens

<220>

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<222> 1..14

<400> 16

Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
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Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15

Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30

Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50

Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65

Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80

Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
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<210> 17

<211> 1175

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..326

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<210> 23
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<213> Homo sapiens
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<222> 10..1212
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18

<222> 1213..1746

<220>

<221> polyA_signal

<222> 1709..1714

<220>

<221> polyA_site

<222> 1733..1746

<400> 23

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      -15                      -10                      -5
tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg 99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
      1                      5                      10
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta 147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
      15                      20                      25                      30
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc 195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
      35                      40                      45
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc 243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
      50                      55                      60
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg 291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
      65                      70                      75
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc 339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
      80                      85                      90
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa 387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
      95                      100                      105                      110
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac 435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
      115                      120                      125
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg 483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
      130                      135                      140
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg 531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
      145                      150                      155
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt 579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
      160                      165                      170
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc 627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
      175                      180                      185                      190
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc 675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
      195                      200                      205
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg 723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
      210                      215                      220
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac 771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
      225                      230                      235
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
      240                      245                      250
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867

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Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
255                               260                               265                               270
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc      915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
                               275                               280                               285
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc      963
Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
                               290                               295                               300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct      1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
                               305                               310                               315
ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca      1059
Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
                               320                               325                               330
gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc      1107
Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
                               335                               340                               345                               350
gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc      1155
Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
                               355                               360                               365
ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc      1203
Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Ile Ser
                               370                               375                               380
ctg ctg aag tgaggaggcc catgggcaga agatagggat tcccctggac      1252
Leu Leu Lys
                               385
cacacctccg tggttcactt tggtcacaag taggagacac agatggcacc tgtggccaga 1312
gcacctcagg accctcccca cccaccaaata gcctctgcct tgatggagaa ggaaaaggct 1372
ggcaagggtgg gttccaggga ctgtacctgt aggagacaga aaagagaaga aagaagcact 1432
ctgctggcgg gaataactctt ggtcacctca aatttaagtc gggaaattct gctgcttgaa 1492
acttcagccc tgaacctttg tcaccattcc tttaaattct ccaaccctaa gtattcttct 1552
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aaaaaaaaaa aaaa
1746

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<210> 24
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 <213> Homo sapiens

<220>
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 <222> 1..17

<400> 24

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Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
      1                               5                               10                               15
Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
      20                               25                               30
Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
      35                               40                               45
Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
      50                               55                               60
Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
      65                               70                               75
Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
      80                               85                               90                               95
Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu
      100                               105                               110
Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu

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			115					120					125				
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr		
		130					135					140					
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met		
		145					150				155						
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr		
160					165				170						175		
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser		
				180					185					190			
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu		
			195					200					205				
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile		
		210					215					220					
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser		
		225				230					235						
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp		
240					245					250				255			
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser		
				260					265					270			
Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val		
			275					280					285				
Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys		
		290					295					300					
His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val		
		305				310					315						
Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu		
320					325					330				335			
Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu		
				340					345					350			
Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg		
			355					360					365				
Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu		
		370					375					380					

Lys

<210> 25
 <211> 1239
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
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 <222> 127..879

<220>
 <221> 3'UTR
 <222> 880..1239

<220>
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 <222> 1224..1239

<400> 25
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 gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag 120
 ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
 -20 -15 -10
 agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216

Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
-5 1 5
Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
10 15 20
Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
25 30 35 40
Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
45 50 55
Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
60 65 70
Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
75 80 85
Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
90 95 100
Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
105 110 115 120
Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
125 130 135
Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
140 145 150
His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
155 160 165
Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
170 175 180
Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
185 190 195 200
Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
205 210 215
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
220 225

<210> 27
<211> 1179
<212> DNA
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<220>
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<220>
<221> CDS
<222> 116..961

<220>
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<222> 962..1179

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<222> 1145..1150

<220>
<221> polyA_site
<222> 1164..1179

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tgggtctctg actcacttct gacttttaggc gctcgaggac tgtgcccagg agcag atg 118
Met
1
cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln

	5	10	15	
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt				214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu				
20	25	30		
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag				262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln				
35	40	45		
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga				310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly				
50	55	60	65	
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat				358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr				
70	75	80		
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct				406
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser				
85	90	95		
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc				454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly				
100	105	110		
ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa				502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys				
115	120	125		
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac				550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp				
130	135	140	145	
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc				598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe				
150	155	160		
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat				646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr				
165	170	175		
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg				694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val				
180	185	190		
cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga				742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg				
195	200	205		
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc				790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly				
210	215	220	225	
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac				838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr				
230	235	240		
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc				886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr				
245	250	255		
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg				934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg				
260	265	270		
cca aat gat ttt att cca aat gta att taattgctgc tgttgggctt				981
Pro Asn Asp Phe Ile Pro Asn Val Ile				
275	280			
tcgtttctgc aattcagctt tgttttaaagt gatttgaaaa atactcattc tgaacatatc				1041
catgcgcaat catgataact gttgtgagta gtgctttttca ttctttctcac ttgcctttgt				1101
tacttaaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg				1161
tcaaaaaaaaa aaaaaaaaa				1179

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 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>

<221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

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 1 5 10 15
 Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
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 Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
 35 40 45
 Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
 50 55 60
 Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
 65 70 75 80
 Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
 85 90 95
 Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
 100 105 110
 Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
 115 120 125
 Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
 130 135 140
 Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
 145 150 155 160
 Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
 165 170 175
 Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 180 185 190
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 195 200 205
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 210 215 220
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 225 230 235 240
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 245 250 255
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 260 265 270
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 275 280

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 <211> 1118
 <212> DNA
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 <222> 1..344

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 <222> 345..1118

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tggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtcc 180
aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cgccccgcag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
Met Gly Arg Thr

cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
-15 -10 -5 1
tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5 10 15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20 25 30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35 40 45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
50 55 60 65
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70 75 80
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85 90 95
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
100 105 110
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115 120 125
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130 135 140 145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
150 155 160
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
165 170 175
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
180 185 190
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
195 200 205
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg
210 215 220 225
gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa 1118
Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys
230 235

<210> 30
<211> 258
<212> PRT
<213> Homo sapiens

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<221> SIGNAL
<222> 1..20

<220>
<221> UNSURE
<222> 49
<223> Xaa = Glu, *

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-20 -15 -10 -5
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1 5 10
Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
15 20 25
Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
30 35 40
Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
45 50 55 60
Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
65 70 75
Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
80 85 90
Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
95 100 105
Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
110 115 120
Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
125 130 135 140
Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
145 150 155
Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
160 165 170
Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
175 180 185
Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
190 195 200
Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
205 210 215 220
Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
225 230 235
Lys Lys

<210> 31
<211> 1273
<212> DNA
<213> Homo sapiens

<220>
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<222> 1..13

<220>
<221> CDS
<222> 14..1048

<220>
<221> 3'UTR
<222> 1049..1273

<220>
<221> polyA_signal


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260          265          270          275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat 961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His
          280          285          290
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa 1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
          295          300          305
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg 1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys
          310          315          320
attggacagt agtgggtgcat ctgggtccttg ccgcctgaga gcccaggag acatcggcta 1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc 1178
agctgtgtcc cccagtcctg gtcttttttag aatgtgaatg atgataaagt tgtgaaataa 1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaa 1273

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<210> 32
 <211> 345
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..26

<400> 32

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-25          -20          -15
Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
-10          -5          1          5
Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
          10          15          20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
          25          30          35
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
          40          45          50
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
55          60          65          70
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
          75          80          85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
          90          95          100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
          105          110          115
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
          120          125          130
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
135          140          145          150
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
          155          160          165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
          170          175          180
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
          185          190          195
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
          200          205          210
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
215          220          225          230
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
          235          240          245
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
          250          255          260
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
          265          270          275

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Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

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 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
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 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
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 <222> 708..723

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 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
 130 135 140
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
 Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys

<221> polyA_signal
<222> 809..814

<220>
<221> polyA_site
<222> 830..845

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taaattctgc caaaaggact gaggaacggg gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
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cagtttatta tcgcaaaaaa aaaaaaaaaa 845

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<211> 179
<212> PRT
<213> Homo sapiens

<400> 36
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Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60

Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
Leu Leu Met Ser Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
Gly Pro Tyr

<210> 37
<211> 517
<212> DNA
<213> Homo sapiens

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<222> 1..16

<220>
<221> CDS
<222> 17..259

<220>
<221> 3'UTR
<222> 260..517

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Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
1 5 10
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
15 20 25
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
30 35 40
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
45 50 55 60
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
65 70 75
gga caa gaa ata gcc tgaccatgag gaccagggag ctgctacccc tccctacagc 299
Gly Gln Glu Ile Ala
80
tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcaccc 359
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419
tttctccaat ggacatgatt cccaagtcat cctgctgcct tttttcttat agacacaatg 479
aacagaccac ccacaacctt agttctctaa gtcaccc 517

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<212> PRT
<213> Homo sapiens

<400> 38

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 Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
 20 25 30
 Phe Val Cys Trp Arg Lys Ile Lys Ser Cys Glu Glu Glu Asn Ala
 35 40 45
 Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
 50 55 60
 Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
 65 70 75 80
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<210> 39
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 gcctcacttc gtcccactgt ggtaggggt gagtctgctg aatgttaagt gatttgctca 180
 aggtgccccat ttcgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
 aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
 -15 -10
 ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
 Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
 -5 1 5
 atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
 Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
 10 15 20
 ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
 Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
 25 30 35 40
 gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg ccc 484
 Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro
 45 50 55
 aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
 Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
 60 65 70
 gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat 580
 Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
 75 80 85

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gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc 628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
90 95 100
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc 676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
105 110 115 120
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc 724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
125 130 135
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc 772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
140 145 150
att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc 820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
155 160 165
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc 868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
170 175 180
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg 916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
185 190 195 200
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag 964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
205 210 215
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac 1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
220 225 230
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgctc 1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
235 240
tcccaagaac agagcctgtc cccagatgtc ccagtagcga tgagtaacag aggtggctgt 1118
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gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cacctgggtc 1718
ccatgaccag ctccccgtct ccataggggt aggcatttca ctggtttatg aagctcgagt 1778
ttcattaaat atgttaagaa tcaaaaaaaaa aaaaaaaaa 1816

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 <213> Homo sapiens

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 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys

45 50 55 60
 Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
 65 70 75
 Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
 80 85 90
 Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
 95 100 105
 Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
 110 115 120
 Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
 125 130 135 140
 Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
 145 150 155
 Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
 160 165 170
 Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
 175 180 185
 Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
 190 195 200
 Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
 205 210 215 220
 Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
 225 230 235
 Arg Gln Pro Tyr Lys Ser Trp
 240

<210> 41
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 <212> DNA
 <213> Homo sapiens

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<220>
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 cacacctgca ccccgcccgg gcatagcacc atg cct gct tgt cgc cta ggc ccg 114
 Met Pro Ala Cys Arg Leu Gly Pro
 -25
 cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162
 Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu
 -20 -15 -10
 gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210
 Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln
 -5 1 5 10
 gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258


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agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
                                         Met Gln Gly
                                         -30
act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
-25 -20 -15
aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
-10 -5 1
aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
5 10 15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20 25 30 35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
40 45 50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
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 <211> 91
 <212> PRT
 <213> Homo sapiens

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 <222> 1..33

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-15 -10 -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
1 5 10 15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
20 25 30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
35 40 45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
50 55

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<400> 45

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cggcccggtt caccgccgagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
                                Met Thr Pro Ser Glu Gly
                                1           5
gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
                                10           15           20
gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
                                25           30           35
cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
                                40           45           50
caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
                                55           60           65           70
ggg ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
                                75           80           85
aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
                                90           95           100
ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
                                105           110           115
gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Leu Arg Leu Pro
                                120           125           130
tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
                                135           140           145           150
tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
                                155           160           165
cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
                                170           175           180
ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
                                185           190           195
gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr
                                200           205           210
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg 787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly
                                215           220           225           230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta 835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val
                                235           240           245
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt 883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly
                                250           255           260
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga 931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly
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Phe

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<210> 46

<211> 279

<212> PRT

<213> Homo sapiens

<400> 46

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          20          25          30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys
          35          40          45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser
          50          55          60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu
65          70          75          80
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu
          85          90          95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys
          100          105          110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp
          115          120          125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala
          130          135          140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Val Gly Lys
          145          150          155          160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro
          165          170          175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly
          180          185          190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln
          195          200          205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser
          210          215          220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp
          225          230          235          240
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys
          245          250          255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly
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Trp Gly Trp Gly Gln Gly Phe
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<210> 47

<211> 1294

<212> DNA

<213> Homo sapiens

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<221> CDS

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<220>

<221> polyA_site

<222> 1279..1294

<400> 47

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ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
Met Ile Tyr Thr Met Lys Lys Val His
-25 -20
gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
Ala Leu Trp Ala Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro
-15 -10 -5
ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
1 5 10
acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15 20 25 30
gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
35 40 45
att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
50 55 60
aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
65 70 75
aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
80 85 90
cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
95 100 105 110
gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
115 120 125
aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
130 135 140
cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
145 150 155
act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc 869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
160 165 170
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag 917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
175 180 185 190
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag 965
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
195 200 205
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa 1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
210 215 220
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga 1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
225 230 235
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata 1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
240 245 250
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttgtt atagcaatgt 1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
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255 260
aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tatttttctt 1219
ctaaaatgct ttttaattaat atgttcatta aattttctat gcttattgta cttgttacca 1279
aaaaaaaaaa aaaaa 1294

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<213> Homo sapiens

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<222> 1..28

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-10 -5 1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5 10 15 20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
25 30 35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
40 45 50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
55 60 65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
70 75 80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85 90 95 100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
105 110 115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
120 125 130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
135 140 145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
150 155 160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165 170 175 180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
185 190 195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
200 205 210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
215 220 225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
230 235 240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245 250 255 260
Lys Asn Met

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<222> 1179..1194

<400> 49
ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct 56
Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20 -15 -10 -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
1 5 10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
15 20 25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
30 35 40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
45 50 55 60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
65 70 75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
80 85 90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
95 100 105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
110 115 120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
125 130 135 140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
145 150 155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
160 165 170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
175 180 185
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
190 195 200
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu
205 210 215 220

				45					50					55				
tat	ggg	gga	tgt	gaa	gga	aat	cag	aat	cga	ttt	gaa	agt	ctg	gaa	gag			586
Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser	Leu	Glu	Glu			
			60					65					70					
tgc	aaa	aaa	atg	tgt	aca	aga	gaa	aag	cca	gat	ttc	tgc	ttt	ttg	gaa			634
Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys	Phe	Leu	Glu			
		75					80				85							
gaa	gat	cct	gga	ata	tgt	cga	ggg	tat	att	acc	agg	tat	ttt	tat	aac			682
Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr	Phe	Tyr	Asn			
	90					95					100							
aat	cag	aca	aaa	cag	tgt	gaa	cgt	ttc	aag	tat	ggg	gga	tgc	ctg	ggc			730
Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly	Cys	Leu	Gly			
	105				110					115				120				
aat	atg	aac	aat	ttt	gag	aca	ctg	gaa	gaa	tgc	aag	aac	att	tgt	gaa			778
Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu			
				125				130					135					
gat	ggg	ccg	aat	ggg	ttc	cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat			826
Asp	Gly	Pro	Asn	Gly	Phe	Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn			
		140						145					150					
gct	gtg	aat	aac	tcc	ctg	act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt			874
Ala	Val	Asn	Asn	Ser	Leu	Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu			
		155						160					165					
ttt	gaa	ttt	cac	ggg	ccc	tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga			922
Phe	Glu	Phe	His	Gly	Pro	Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly			
	170					175				180								
ttg	tgt	cgt	gcc	aat	gag	aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg			970
Leu	Cys	Arg	Ala	Asn	Glu	Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly			
	185				190				195				200					
aaa	tgc	cgc	cca	ttt	aag	tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat			1018
Lys	Cys	Arg	Pro	Phe	Lys	Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn			
			205					210					215					
ttt	act	tcc	aaa	caa	gaa	tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc			1066
Phe	Thr	Ser	Lys	Gln	Glu	Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile			
		220						225					230					
caa	aga	ata	tca	aaa	gga	ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag			1114
Gln	Arg	Ile	Ser	Lys	Gly	Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys			
	235						240					245						
aag	cag	aga	gtg	aaa	ata	gca	tat	gaa	gaa	att	ttt	gtt	aaa	aat	atg			1162
Lys	Gln	Arg	Val	Lys	Ile	Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met			
	250					255					260							
tgaattt	gtt	atagca	atgt	aacatta	at	ctactaa	ata	ttttat	atga	aatgttt	cac							1222
tatgatt	ttc	tattttt	ctt	ctaaa	atgct	tttaatta	at	atgttc	atta	aattttt	ctat							1282
gcttatt	gta	cttggt	atca	aaaaaaaa	aaaaa													1317

<210> 52
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 52
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
 -25 -20 -15
 Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu


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1           5           10           15
Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
20           25           30
Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
35           40           45
Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
50           55           60
Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
65           70           75           80
Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
85           90           95
Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
100          105          110
Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
115          120          125
Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
130          135          140
His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
145          150          155          160
Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
165          170          175
Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
180          185          190
Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
195          200          205

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<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..25

<220>
 <221> CDS
 <222> 26..628

<220>
 <221> 3'UTR
 <222> 629..809

<220>
 <221> polyA_signal
 <222> 766..771

<220>
 <221> polyA_site
 <222> 795..809

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<400> 55
agaaaggtgt gggtggcatg gggca atg ctt gag gta tca gat gca ctg gga      52
                               Met Leu Glu Val Ser Asp Ala Leu Gly
                               1           5
gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac      100
Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
10           15           20           25
acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga      148
Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
30           35           40
aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct      196
Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro

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      45      50      55
ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc 244
Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser
      60      65      70
ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292
Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val
      75      80      85
ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340
Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala
      90      95      100      105
tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388
Ser Val Phe Ser Glu Gln Ala Cys Pro Ser Leu Lys Ile Glu Tyr Ala
      110      115      120
ttt cgc atc tat gat ttt aat gag aat ggc ttc att gat gag gag gat 436
Phe Arg Ile Tyr Asp Phe Asn Glu Asn Gly Phe Ile Asp Glu Glu Asp
      125      130      135
ctg cag agg atc atc ctg cga ctg ctg aac agt gat gac atg tct gag 484
Leu Gln Arg Ile Ile Leu Arg Leu Leu Asn Ser Asp Asp Met Ser Glu
      140      145      150
gac ctc ctg atg gac ctc acg aac cac gtc ctg agt gag tcg gat ctg 532
Asp Leu Leu Met Asp Leu Thr Asn His Val Leu Ser Glu Ser Asp Leu
      155      160      165
gac aat gac aac atg ctg tcc ttc tca gag ttt gaa cat gca atg gcc 580
Asp Asn Asp Asn Met Leu Ser Phe Ser Glu Phe Glu His Ala Met Ala
      170      175      180      185
aag tct cca gat ttc atg aac tcc ttt cgg att cac ttc tgg gga tgc 628
Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys
      190      195      200
tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaacccc 688
ctccagcact ggagggagct ggtttgaagt atgactttgt actgggcccac cactcacctc 748
tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaaaa aaaaaaaaaa 808
t 809

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<210> 56
 <211> 201
 <212> PRT
 <213> Homo sapiens

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<400> 56
Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly
1      5      10      15
Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu
      20      25      30
Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His
      35      40      45
Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Tyr Lys Glu Ala
      50      55      60
Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn
      65      70      75      80
Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe
      85      90      95
Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala
      100      105      110
Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn
      115      120      125
Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg
      130      135      140
Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr
      145      150      155      160
Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser
      165      170      175
Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn
      180      185      190

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Ser Phe Arg Ile His Phe Trp Gly Cys
 195 200

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
 <221> 3'UTR
 <222> 965..1133

<220>
 <221> polyA_signal
 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
 gacataatca gagctatgct ggaggagaag agggcagcca tttgctggct ggcttgcaat 60
 gagccaggag gtggcaggac gagttaggag gctgggttcag tagctcgggc aagagcaggg 120
 cccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaagggt cgaccaggga tttcaaggcc agccaggctt 240
 tccgggcccc ccgggtcccc ctggattccc aggcacaagt ggatcacctg gcccacctgg 300
 ccctcaagca gagaagggtc gcgaagggtat tcgaggccca tcaggcctgc ctggctcccc 360
 tgggccaccg ggacctcctg ggattcagggt cccgcgcggg ctggatgggt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggctcctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
 85 90 95
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
 100 105 110
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
 115 120 125

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cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
130          135          140          145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
          150          155          160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacaggttg tgaatgtttt ttttgttggt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

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<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

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<400> 58
Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro
1          5          10          15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
          20          25          30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
          35          40          45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
          50          55          60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
          65          70          75          80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
          85          90          95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
          100          105          110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
          115          120          125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
          130          135          140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
          145          150          155          160
Pro Phe Gly

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```

<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..78

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<220>
<221> CDS
<222> 79..642

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<220>
<221> 3'UTR
<222> 643..838

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<220>
<221> polyA_signal
<222> 799..804

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<220>
<221> polyA_site
<222> 823..838

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<400> 59

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aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggtc 60
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
                Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
                1          5          10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
                15          20          25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
                30          35          40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
                45          50          55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
                60          65          70          75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
                80          85          90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
                95          100          105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
                110          115          120
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
                125          130          135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
                140          145          150          155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
                160          165          170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
                175          180          185
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccacacct 692
Lys
gaccctccc tcagctgtcc tgtgccccgc cctctccgc acactcagtc cccctgctg 752
gcgttccctgc cgcagctctg acctgggtgct gtcgccctgg catcttaata aamcctgctt 812
atacttcctt aaaaaaaaaa aaaaaa 838

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<210> 60

<211> 188

<212> PRT

<213> Homo sapiens

<400> 60

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Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1          5          10          15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
                20          25          30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
                35          40          45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
                50          55          60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
                65          70          75          80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
                85          90          95

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Thr	Glu	Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Lys	Val	Met	Arg	Trp	Phe
			100					105					110		
Gln	Ala	Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala
		115					120					125			
Trp	Val	Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu
		130				135					140				
Trp	Lys	Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met
145					150					155				160	
Ser	Ser	Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu
				165					170					175	
Thr	Pro	Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys				
			180					185							

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
 attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60
 tggctgctgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120
 ccgctgcagg cagcagcagc ccccgccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
 85 90 95
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
 100 105 110
 ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
 Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
 115 120 125 130

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cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
          135          140          145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
          150          155          160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
          165          170          175
ttc ggg atc gtg tagccggcgg ggcggggggcc gtgggggggccc tggaggagggg 804
Phe Gly Ile Val
          180
caggagccgc gggaggcccg gaggaggggtg gggaccttgc agcccccatc ctctccgt 862

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<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..21

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<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
  -20          -15          -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
  -5          1          5          10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
          15          20          25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
          30          35          40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
          45          50          55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
          60          65          70          75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
          80          85          90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
          95          100          105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
          110          115          120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
          125          130          135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
          140          145          150          155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
          160          165          170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
          175          180

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<210> 63
<211> 618
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..194

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<220>
<221> CDS
<222> 195..587

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<220>
 <221> 3'UTR
 <222> 588..618

<220>
 <221> polyA_signal
 <222> 578..583

<220>
 <221> polyA_site
 <222> 604..618

<400> 63
 atttgcttag gtctgatcaa tctgctccac acaattttctc agtgatcctc tgcattctctg 60
 cctacaagggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
 ttcgtttttac cttgatctct ctctgacaaa gaaatccaga tgatgagaga cctgatgaag 180
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
 -20 -15 -10
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
 -5 1 5
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
 10 15 20
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
 25 30 35
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
 40 45 50 55
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
 Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
 60 65 70
 atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
 Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
 75 80 85
 act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
 Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
 90 95 100
 tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
 Cys Phe Ala Leu Leu Asn Cys
 105 110

<210> 64
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

<400> 64
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 -5 1 5 10
 Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40

Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 60 65 70
 Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala
 75 80 85 90
 Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu
 95 100 105
 Leu Asn Cys

<210> 65
 <211> 836
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..176

<220>
 <221> CDS
 <222> 177..767

<220>
 <221> 3'UTR
 <222> 768..836

<220>
 <221> polyA_signal
 <222> 814..819

<220>
 <221> polyA_site
 <222> 822..836

<400> 65
 aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgcctacaag ggccctccctg 60
 acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179
 Met
 aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
 -20 -15 -10 -5
 gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
 Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
 1 5 10
 gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
 Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
 15 20 25
 gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
 Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
 30 35 40
 gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
 Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
 45 50 55 60
 tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
 Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
 65 70 75
 tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
 Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
 80 85 90
 atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
 Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu

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          95              100              105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
    110              115              120
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
    125              130              135              140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
          145              150              155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
          160              165              170
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaaatatg 807
Phe Ser Pro Ala
          175
atagtgtata aatgaaaaaa aaaaaaaaaa 836

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<210> 66
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..22

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<400> 66
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
    -20              -15              -10
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
    -5              1              5              10
Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
          15              20              25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
          30              35              40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
          45              50              55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
          60              65              70
Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
    75              80              85              90
Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
          95              100              105
Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
          110              115              120
Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
          125              130              135
Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
          140              145              150
Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
    155              160              165              170
Leu Phe Ser Pro Ala
          175

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<210> 67
 <211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

<400> 67
 atatgtcatc agggccccccg cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggt 652
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
 gaaaaaaaa aaaaaaa 789

<210> 68
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 68

Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly		
385						390					395						
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356	
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala		
400					405					410					415		
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404	
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser		
				420					425					430			
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452	
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu		
				435					440					445			
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	act	tta	atc	1500	
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile		
				450					455					460			
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548	
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp		
				465					470					475			
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596	
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser		
480					485					490					495		
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644	
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp		
				500						505					510		
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692	
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys		
				515					520					525			
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740	
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr		
				530					535					540			
cga	aag	cct	ttc	cat	caa	gaa	aat	ggg	gat	gtg	att	tat	gct	ttc	gta	1788	
Arg	Lys	Pro	Phe	His	Gln	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val			
					545				550					555			
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836	
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val		
560					565					570					575		
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884	
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg		
				580					585					590			
gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932	
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser		
				595					600					605			
gca	cat	gtt	tgt	tca	caa	cag	tgt	tct	gga	cat	gga	gtg	tgt	gat	tcc	1980	
Ala	His	Val	Cys	Ser	Gln	Gln	Cys	Ser	Gly	His	Gly	Val	Cys	Asp	Ser		
				610					615					620			
aga	aac	aag	tgc	cat	tgt	tcg	cca	ggc	tat	aag	cct	cca	aac	tgc	caa	2028	
Arg	Asn	Lys	Cys	His	Cys	Ser	Pro	Gly	Tyr	Lys	Pro	Pro	Asn	Cys	Gln		
				625					630					635			
ata	cgt	tcc	aaa	gga	ttt	tcc	ata	ttt	cct	gag	gaa	gat	atg	ggg	tca	2076	
Ile	Arg	Ser	Lys	Gly	Phe	Ser	Ile	Phe	Pro	Glu	Glu	Asp	Met	Gly	Ser		
640					645					650					655		
atc	atg	gaa	aga	gca	tct	ggg	aag	act	gaa	aac	acc	tgg	ctt	cta	ggg	2124	
Ile	Met	Glu	Arg	Ala	Ser	Gly	Lys	Thr	Glu	Asn	Thr	Trp	Leu	Leu	Gly		
				660					665					670			
ttc	ctc	att	gct	ctt	cct	att	ctc	att	gta	aca	acc	gca	ata	gtt	ttg	2172	
Phe	Leu	Ile	Ala	Leu	Pro	Ile	Leu	Ile	Val	Thr	Thr	Ala	Ile	Val	Leu		
				675					680					685			
gca	agg	aaa	cag	ttg	aaa	aac	tgg	tct	gcc	aag	gaa	gag	gaa	ttc	cca	2220	
Ala	Arg	Lys	Gln	Leu	Lys	Asn	Trp	Phe	Ala	Lys	Glu	Glu	Glu	Phe	Pro		
				690					695					700			
agt	agc	gaa	tct	aaa	tcg	gaa	ggg	agc	aca	cag	aca	tat	gcc	agc	caa	2268	
Ser	Ser	Glu	Ser	Lys	Ser	Glu	Gly	Ser	Thr	Gln	Thr	Tyr	Ala	Ser	Gln		
				705					710					715			
tcc	agc	tca	gaa	ggc	agc	act	cag	aca	tat	gcc	ggc	caa	acc	aga	tca	2316	

Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
 720 725 730 735
 gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
 Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
 740 745 750
 gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
 Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
 755 760 765
 caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
 Gln Ser Ser Ser Asn
 770
 tcgctaagaa atgaaaattc tgtcttttcc tccgtgggtca cagctgaaag aaacaataaa 2527
 ttgagtgtgg accaaaaaaa aaaaaaaat 2556

<210> 70
 <211> 787
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 70
 Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
 -15 -10 -5
 Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
 1 5 10 15
 Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
 20 25 30
 Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
 35 40 45
 Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
 50 55 60
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
 65 70 75 80
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
 85 90 95
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
 100 105 110
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
 115 120 125
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
 130 135 140
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
 145 150 155 160
 Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
 165 170 175
 Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
 180 185 190
 Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
 195 200 205
 Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
 210 215 220
 Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
 225 230 235 240
 Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
 245 250 255
 Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
 260 265 270
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
 275 280 285
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr

290		295		300
Gln Met Leu Ala Leu Ser	Leu Gly Ile Ser Tyr	Asp Asp Pro Lys Lys		
305	310	315		320
Cys Gln Cys Ser Glu Ser Thr Cys Ile Met	Asn Pro Glu Val Val Gln			
	325	330		335
Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser	Leu Arg Ser Phe Gln			
	340	345		350
Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu	Gln Asn Lys Pro Gln			
	355	360		365
Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly	Asn Gly Arg Leu Glu			
	370	375		380
Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala	Gln Cys Gly Pro Ala			
385	390	395		400
Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys	Asp Gly Ala Lys Cys			
	405	410		415
Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile	Leu Gln Ser Gly Val			
	420	425		430
Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp	Ile Ala Glu Asn Cys			
	435	440		445
Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile	Thr Leu Ile Asn Gly			
	450	455		460
Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr	Asp Gly Asp Cys His			
465	470	475		480
Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly	Lys Gly Ser Arg Asn			
	485	490		495
Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser	Gln Ser Asp Arg Phe			
	500	505		510
Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr	Val Phe Cys Gly Trp			
	515	520		525
Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr	Tyr Pro Thr Arg Lys			
	530	535		540
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr	Ala Phe Val Arg Asp			
545	550	555		560
Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro	Arg Thr Val Pro Asp			
	565	570		575
Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp	Ile Gly Arg Val Cys			
	580	585		590
Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile	Lys Ala Ser Ala His			
	595	600		605
Val Cys Ser Gln Gln Cys Ser Gly His Gly Val	Cys Asp Ser Arg Asn			
	610	615		620
Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro	Asn Cys Gln Ile Arg			
625	630	635		640
Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp	Met Gly Ser Ile Met			
	645	650		655
Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp	Leu Leu Gly Phe Leu			
	660	665		670
Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala	Ile Val Leu Ala Arg			
	675	680		685
Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu	Glu Phe Pro Ser Ser			
	690	695		700
Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr	Ala Ser Gln Ser Ser			
705	710	715		720
Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln	Thr Arg Ser Glu Ser			
	725	730		735
Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser	Glu Asp Ser Ala Glu			
	740	745		750
Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser	Thr Gln Thr Gln Ser			
	755	760		765
Ser Ser Asn				
770				

<210> 71

<211> 1603
 <212> DNA
 <213> Homo sapiens

<220>
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<220>
 <221> CDS
 <222> 8..763

<220>
 <221> 3'UTR
 <222> 764..1603

<220>
 <221> polyA_signal
 <222> 1562..1567

<220>
 <221> polyA_site
 <222> 1588..1603

<400> 71
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 Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu
 -15 -10 -5
 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
 1 5 10
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
 15 20 25 30
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
 35 40 45
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
 50 55 60
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
 65 70 75
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
 80 85 90
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His
 95 100 105 110
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
 115 120 125
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
 130 135 140
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529
 Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala
 145 150 155
 ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577
 Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala
 160 165 170
 ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625
 Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg

160 165 170 175
 Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu
 180 185 190
 Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro
 195 200 205
 Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln
 210 215 220
 Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
 225 230 235

<210> 73
 <211> 879
 <212> DNA
 <213> Homo sapiens

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 <222> 1..8

<220>
 <221> CDS
 <222> 9..395

<220>
 <221> 3'UTR
 <222> 396..879

<220>
 <221> polyA_site
 <222> 864..879

<400> 73
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 Met Ala Val Leu Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly
 -15 -10 -5
 cca ggc ccg ggt cct cgg ccg ctg tgg ggc cca ggc ccg gcc tgg agt 98
 Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
 1 5 10 15
 cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
 Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
 20 25 30
 agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194
 Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
 35 40 45
 tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
 Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
 50 55 60
 ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
 Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
 65 70 75
 tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
 Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
 80 85 90 95
 aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
 Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
 100 105 110
 ata ttc atc tga ttt ctt cag tca gtag ctgcctctgg atgtctttac 435
 Ile Phe Ile
 rtttctgttt wctttttagc aaggtgaaac cagtctggam aatggggaga tgggccgggt 495
 gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
 ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtgggtggc 615
 tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc 675
 caacatggtg aaacccgctc tttaactaaaa atagaaaatt agccgggcgt gatggcacac 735

gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaac 855
tccatcccaa aaaaaaaaaa aaaa 879

<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..16

<400> 74
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-15 -10 -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
1 5 10 15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20 25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50 55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
85 90 95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
100 105 110
Ile

<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..87

<220>
<221> CDS
<222> 88..1269

<220>
<221> 3'UTR
<222> 1270..1634

<220>
<221> polyA_signal
<222> 1594..1599

<220>
<221> polyA_site
<222> 1619..1634

<400> 75
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agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162

Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His
 350 355 360
 ctg gtt cac gaa tta agg cgt cga ggt gga aaa tat gcc gtt gga tca 1218
 Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser
 365 370 375
 gct tgc att gga ggt ggc caa ggt att gct gtc atc att cag agc aca 1266
 Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr
 380 385 390
 gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag 1319
 Ala
 gccacagtaa aacaagtgac cttcagagca gctgccacaa ctggccatgc cctgccattg 1379
 aaacagtgat taagtttgat caagccatgg tgacacaaaa atgcattgat catgaatagg 1439
 agcccatgct agaagtacat tctctcagat ttgaaccagt gaaatatgat gtatttctga 1499
 gctaaaactc aactatagaa gacattaaaa gaaatcgtat tcttgccaag taaccaccac 1559
 ttctgcctta gataatatga ttataaggaa atcaaataaa tgttgcctta acttcaaaca 1619
 aaaaaaaaaa aaaaa 1634

<210> 76

<211> 394

<212> PRT

<213> Homo sapiens

<400> 76

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 1 5 10 15
 Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu Ser Glu Phe
 20 25 30
 Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val
 35 40 45
 Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile
 50 55 60
 Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr
 65 70 75 80
 Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile
 85 90 95
 Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu
 100 105 110
 Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn
 115 120 125
 Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser
 130 135 140
 Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met
 145 150 155 160
 Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys
 165 170 175
 Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp
 180 185 190
 Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys
 195 200 205
 Lys Gly Lys Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr
 210 215 220
 Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly
 225 230 235 240
 Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala
 245 250 255
 Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro
 260 265 270
 Leu Ala Arg Ile Val Gly Tyr Phe Val Ser Gly Cys Asp Pro Ser Ile
 275 280 285
 Met Gly Ile Gly Pro Val Pro Ala Ile Ser Gly Ala Leu Lys Lys Ala
 290 295 300
 Gly Leu Ser Leu Lys Asp Met Asp Leu Val Glu Val Asn Glu Ala Phe
 305 310 315 320

Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser
325 330 335
Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly
340 345 350
Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg
355 360 365
Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln
370 375 380
Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
385 390

<210> 77
<211> 1642
<212> DNA
<213> Homo sapiens

<220>
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<220>
<221> CDS
<222> 69..875

<220>
<221> 3'UTR
<222> 876..1642

<220>
<221> polyA_signal
<222> 1599..1604

<220>
<221> polyA_site
<222> 1627..1642

<400> 77
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taggaatc atg gcg gct gcg ctg ttc gtg ctg ctg gga ttc gcg ctg ctg 110
Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
-20 -15 -10
ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta 158
Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
-5 1 5 10
gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
15 20 25
gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254
Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
30 35 40
aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
45 50 55
gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
60 65 70
ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
75 80 85 90
aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
95 100 105
aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494

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Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
      110      115      120
act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc 542
Thr Asp Ser Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
      125      130      135
ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg 590
Phe Val Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
      140      145      150
aac atg gag gcc gac ccc ggc cag tac cgg tgc aac ggc acc agc tcc 638
Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser
      155      160      165      170
aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg 686
Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
      175      180      185
gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg 734
Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
      190      195      200
gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gac gtc 782
Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
      205      210      215
ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag 830
Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
      220      225      230
cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc 875
His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
      235      240      245
tgaggcaggt ggcccgagga cgctccctgc tccgcgtctg cgccgcccgc ggagtcact 935
cccagtgctt gcaagattcc aagttctcac ctcttaaaga aaaccacccc cgtagattcc 995
catcacacac ttccttcttt tttaaaaaag ttgggttttc tccattcagg attctgttcc 1055
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cgtctgtggc tttcagcctc tgggtctgag tcatggccgg gtgggcggca cagccttctc 1175
cactggccgg agtcagtgcc aggtccttgc cctttgtgga aagtcacagg tcacacgagg 1235
ggcccgtgt cctgcctgtc tgaagccaat gctgtctggt tgcgccattt ttgtgctttt 1295
atgtttaatt ttatgagggc cacgggtctg tgttcgactc agcctcaggg acgactctga 1355
cctcttggcc acagaggact cacttgccca caccgagggc gaccccgcca cagcctcaag 1415
tcaactccaa gcccctcct tgtctgtgca tccgggggca gctctggagg gggtttgctg 1475
gggaactggc gccatcgccg ggactccaga accgcagaag cctccccagc tcacccttg 1535
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<210> 78
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

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<400> 78
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  -20      -15      -10
His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
  -5      1      5      10
Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
      15      20      25
Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
      30      35      40
Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
      45      50      55
Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
      60      65      70      75
Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser

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      80      85      90
Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
      95      100
Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
      110      115      120
Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
      125      130      135
Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
      140      145      150      155
Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
      160      165      170
Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
      175      180      185
Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
      190      195      200
Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
      205      210      215
Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
      220      225      230      235
Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
      240      245

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<210> 79
 <211> 1466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..343

 <220>
 <221> CDS
 <222> 344..1144

 <220>
 <221> 3'UTR
 <222> 1145..1466

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<400> 79
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aattggcagc cttagaacta gtgggaaggc ggggtgcgcga agtcgagggg cggagagagg 120
gggcccggag agctgctttc tgaatccaag ttcgtgggct ctctcagaag tcctcaggac 180
ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240
tctttcggac tcgaatcacg gctgctgcga aggggtctagt tccggacact aggggtgcccg 300
aacgcgctga tgccccgagt gctcgcaggg cttcccgccta acc atg ctg ccg ccg 355
                                     Met Leu Pro Pro
ccg ccg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403
Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu
-25 -20 -15 -10
gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451
Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro
-5 1 5
gat tac ctg ccg cgc ggc tgg atg ccg ctg cta gcg gag ggc gag ggc 499
Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly
10 15 20
tgc gct ccc tgc ccg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547
Cys Ala Pro Cys Arg Pro Glu Cys Ala Ala Pro Arg Gly Cys Leu
25 30 35
gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac 595
Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn
40 45 50 55
ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg 643

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Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala His Phe Tyr Gly
 60 65 70
 cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca ggc ggc gac ctg 691
 His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr Gly Gly Asp Leu
 75 80 85
 agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt cgt tcg cag agt 739
 Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys Arg Ser Gln Ser
 90 95 100
 ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag atc tgc cgc ctg 787
 Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln Ile Cys Arg Leu
 105 110 115
 cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc act gtg gca cac 835
 Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu Thr Val Ala His
 120 125 130 135
 ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca cat cca tat gac 883
 Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser His Pro Tyr Asp
 140 145 150
 act tgg aat gtg aca ggg cag gat gtg atc ttt ggc tgt gaa gtg ttt 931
 Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly Cys Glu Val Phe
 155 160 165
 gcc tac ccc atg gcc tcc atc gag tgg agg aag gat ggc ttg gac atc 979
 Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile
 170 175 180
 cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg ggt gga 1027
 Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly
 185 190 195
 ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct gtg cgt 1075
 Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg
 200 205 210 215
 ccc agt gat gag ggc act tac cgc tgc ctt ggc cca atg ccc tgg gtc 1123
 Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro Met Pro Trp Val
 220 225 230
 aag tgg agg ccc ctg cta gct tgacagtgt cacacctgac cagctgaact 1174
 Lys Trp Arg Pro Leu Leu Ala
 235
 ctacaggcat ccccgactg cgatcactaa acctgggttcc tgaggaggag gctgagagtg 1234
 aagagaatga cgattactac taggtccaga gctctggccc atgggggtgg gtgagcggct 1294
 atagtgttca tccctgctct tgaaaagacc tggaaagggg agcagggtcc cttcatcgac 1354
 tgctttcatg ctgtcagtag ggatgatcat gggaggccta tttgactcca aggtagcagt 1414
 gtggtaggat agagacaaaa gctggaggag ggtagggaga gaagctgaga cc 1466

 <210> 80
 <211> 267
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> 1..30

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 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Thr Gly Ala Arg Pro
 -10 -5 1
 Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
 5 10 15
 Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
 20 25 30
 Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
 35 40 45 50
 Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
 55 60 65

<211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
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<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

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<400> 85
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gcggttcgcc ccgcagcctc gccccctgcc cccccgggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
          -20          -15          -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10          15          20          25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
          30          35          40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
          75          80          85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
          90          95          100          105
ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550
Gly Pro Ser
acagacattc gggagacggc ctctgtgttc gccatcactg cggccggcgc cagccacgcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggccccctc cccggccctc cggcctgccc ggcacccccg gacccccctgg ccccgcgggc 730
tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg cctgtcggag ccacacgcgc 910
accgagtgca aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttgcgcagggt gggcgcgcgg ctgctggagc gcttycacgg cgcctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgcgc tccgcacgct caagccgccc 1090
ggccgagcgg acctcctcta cgccgccgat tcgcccgcact tctgcgcccc caaccgacgc 1150

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accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcggggcac cgccaggaga gcgtgcagct cgaagagAAC 1270
tgectgtgcc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccgcc cggccgctag actgacttcg cgcagcgggtg 1390
gctcgcacct gtgggacctc agggcacccg caccggggcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccgaggcg ccagacggcc ccgaaaaggc gctcgggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttggcc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
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aaaa                                              1754

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<210> 86
 <211> 131
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

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<400> 86
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Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5                      1                      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
          10                      15                      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
          75          80          85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
          90          95          100
Gly Pro Ser
105

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<210> 87
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
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 <222> 1399..1404

<220>

<221> polyA_site

<222> 1416..1431

<400> 87

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gccccaaacca agggccccag agagggtcccc caggccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1             5

cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
              10              15              20

gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
              25              30              35

cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
              40              45              50              55

tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
              60              65              70

ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
              75              80              85

gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
              90              95              100

gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
              105              110              115

ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
              120              125              130              135

tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
              140              145              150

agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
              155              160              165

aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr

tccccagaaa ccactctat cctcaccctg ttttgtgtc ttccctcgc ctgctagggc 765
tgcggttct gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
ggctgatacc cagagaacct gggcacttgc tgctgatgc ccaccctgc cagtcattcc 885
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gaccacagg gcaggacct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
cttagatect tttctacca ctttcctatg gaggattcca agtcaccact tctctcaccg 1125
gcttctacca gggccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
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tgttgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccaggtt ttccttgctc cccagctgct ctgccccttt ccccttcttc 1365
cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431
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<210> 88

<211> 168

<212> PRT

<213> Homo sapiens

<400> 88

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Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
35 40 45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
50 55 60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65 70 75 80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
85 90 95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
100 105 110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
115 120 125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
130 135 140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145 150 155 160
Pro Ser Pro Ser Glu Pro Gly Thr
165

<210> 89
<211> 1431
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..151

<220>
<221> CDS
<222> 152..655

<220>
<221> 3'UTR
<222> 656..1431

<220>
<221> polyA_signal
<222> 1399..1404

<220>
<221> polyA_site
<222> 1416..1431

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gcccaaacca aggcccccag agaggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
Met Leu Phe Arg Leu Ser Glu
1 5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
10 15 20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
25 30 35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
40 45 50 55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu

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        60              65              70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
        75              80              85
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
        90              95              100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
        105              110              115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
        120              125              130              135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
        140              145              150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
        155              160              165
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Thr
tccccagaaa cccactctat cctcaccctg ttttgtgctc ttcccctcgc ctgctagggc 765
tgcggtttct gacttctaga agactaaggc tgggtctgtgt ttgcttgttt gccacacctt 825
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gacccacagg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
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gcttctacca ggggtccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
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cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa 1431

<210> 90
<211> 168
<212> PRT
<213> Homo sapiens

<400> 90
Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1 5 10 15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
20 25 30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
35 40 45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
50 55 60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65 70 75 80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
85 90 95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
100 105 110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
115 120 125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
130 135 140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145 150 155 160
Pro Ser Pro Ser Glu Pro Gly Thr
165

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<210> 91
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 <213> Homo sapiens

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<220>
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 <222> 48..1301

<220>
 <221> 3'UTR
 <222> 1302..1417

<220>
 <221> polyA_signal
 <222> 1360..1365

<220>
 <221> polyA_site
 <222> 1402..1417

<400> 91
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 Met Pro Ser
 tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
 Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
 -20 -15 -10 -5
 cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca 152
 Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
 1 5 10
 gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc 200
 Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
 15 20 25
 ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac 248
 Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
 30 35 40
 cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca 296
 Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
 45 50 55 60
 gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa 344
 Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 65 70 75
 atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag 392
 Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 80 85 90
 atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac 440
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 95 100 105
 agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc 488
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 110 115 120
 ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac 536
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 125 130 135 140
 tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa 584
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 145 150 155
 cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat 632

Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys	Ile	Val	Asp	
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Leu	Val	Lys	Glu	Leu	Asp	Arg	Asp	Thr	Val	Phe	Ala	Leu	Val	Asn	Tyr	
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atc	ttc	ttt	aaa	ggc	aaa	tgg	gag	aga	ccc	ttt	gaa	gtc	aag	gac	acc	728
Ile	Phe	Phe	Lys	Gly	Lys	Trp	Glu	Arg	Pro	Phe	Glu	Val	Lys	Asp	Thr	
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gag	gaa	gag	gac	ttc	cac	gtg	gac	cag	gcg	acc	acc	gtg	aag	gtg	cct	776
Glu	Glu	Glu	Asp	Phe	His	Val	Asp	Gln	Ala	Thr	Thr	Val	Lys	Val	Pro	
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atg	atg	aag	cgt	tta	ggc	atg	ttt	aac	atc	cag	cac	tgt	aag	aag	ctg	824
Met	Met	Lys	Arg	Leu	Gly	Met	Phe	Asn	Ile	Gln	His	Cys	Lys	Lys	Leu	
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tcc	agc	tgg	gtg	ctg	ctg	atg	aaa	tac	ctg	ggc	aat	gcc	acc	gcc	atc	872
Ser	Ser	Trp	Val	Leu	Leu	Met	Lys	Tyr	Leu	Gly	Asn	Ala	Thr	Ala	Ile	
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ttc	ttc	ctg	cct	gat	gag	ggg	aaa	cta	cag	cac	ctg	gaa	aat	gaa	ctc	920
Phe	Phe	Leu	Pro	Asp	Glu	Gly	Lys	Leu	Gln	His	Leu	Glu	Asn	Glu	Leu	
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acc	cac	gat	atc	atc	acc	aag	ttc	ctg	gaa	aat	gaa	gac	aga	agg	tct	968
Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser	
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gcc	agc	tta	cat	tta	ccc	aaa	ctg	tcc	att	act	gga	acc	tat	gat	ctg	1016
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu	
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aag	agc	gtc	ctg	ggc	caa	ctg	ggc	atc	act	aag	gtc	ttc	agc	aat	ggg	1064
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly	
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gct	gac	ctc	tcc	ggg	gtc	aca	gag	gag	gca	ccc	ctg	aag	ctc	tcc	aag	1112
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys	
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gcc	gtg	cat	aag	gct	gtg	ctg	acc	atc	gac	gag	aaa	ggg	act	gaa	gct	1160
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala	
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gct	ggg	ggc	atg	ttt	tta	gag	gcc	ata	ccc	atg	tct	atc	ccc	ccc	gag	1208
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu	
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gtc	aag	ttc	aac	aaa	ccc	ttt	gtc	ttc	tta	atg	att	gaa	caa	aat	acc	1256
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Glu	Gln	Asn	Thr	
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aag	tct	ccc	ctc	ttc	atg	gga	aaa	gtg	gtg	aat	ccc	acc	caa	aaa		1301
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys		
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taaagaagggt ttgagctggc cctgcctgc atgtgactgc aaaaaaaaaa aaaaaa															1417	

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<210> 92
<211> 418
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> 1..24
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<400> 92															
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				-20					-15					-10	
Cys	Leu	Val	Pro	Val	Ser	Leu	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Ala	Ala
			-5					1				5			
Gln	Lys	Thr	Asp	Thr	Ser	His	His	Asp	Gln	Asp	His	Pro	Thr	Phe	Asn
	10					15					20				

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 25 30 35 40
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 45 50 55
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 60 65 70
 His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
 75 80 85
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 90 95 100
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 105 110 115 120
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
 125 130 135
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
 140 145 150
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
 155 160 165
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 170 175 180
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 185 190 195 200
 Lys Asp Thr Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val
 205 210 215
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 220 225 230
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 235 240 245
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 250 255 260
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 265 270 275 280
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 285 290 295
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 300 305 310
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 315 320 325
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 330 335 340
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 345 350 355 360
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 365 370 375
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 380 385 390
 Gln Lys

<210> 93
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..277

<220>
 <221> CDS
 <222> 278..733

<220>
 <221> 3'UTR

<222> 734..1115

<220>

<221> polyA_signal

<222> 1072..1077

<220>

<221> polyA_site

<222> 1101..1115

<400> 93

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ctcttttgctc taacagacag cagcgacttt aggctggata atagtcaa at tcttacctcg 60
ctcttttcaact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacaa aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
                               Met His Phe Gly Leu Leu
                               -15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
                               -10                               -5                               1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5                               10                               15                               20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
                               25                               30                               35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
                               40                               45                               50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55                               60                               65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70                               75                               80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85                               90                               95                               100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105                               110                               115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120                               125                               130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783
Ala Ile
ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaac aaatgatggt 903
tggaagaatg cggctcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatatttggt cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atattttacat gcataggaaa aaaaaaaaaa aa 1115
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<210> 94

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

20	25	30	
cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga			483
Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg			
35	40	45	50
cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga			531
Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg			
	55	60	65
ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca			579
Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala			
	70	75	80
aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc			627
Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys			
	85	90	95
ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat			675
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr			
	100	105	110
ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga			723
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly			
	115	120	125
130			
tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg			774
Cys Leu Gly Asn Gln Gln Phe			
	135		
tgaagatggg ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa			834
taactccctg actccgcaat caaccaagggt tcccagcctt tttgaatttc acgggtccctc			894
atgggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta			954
caattcagtc attgggaaat gccgccatt taagtacagt ggatgtgggg gaaatgaaaa			1014
caattttact tccaaacaag aatgtctgag ggcattgtaaa aaagggtttca tccaaagaat			1074
atcaaaagga ggcctaatta aaacaaaaag aaaaagaaag aagcagagag tgaaaatagc			1134
atatgaagaa atttttgtta aaaatatgtg aattttgttat agcaatgtaa cattaattct			1194
actaaatatt ttatatgaaa tgtttcacta tgattttcta tttttcttct aaaatgcttt			1254
taattaatat gttcattaaa ttttctatgc ttattgcaaa aaaaaaaaaaaa aaa			1307

<210> 96
 <211> 164
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 96
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
 -25 -20 -15
 Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
 40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
 70 75 80
 Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
 85 90 95 100
 Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
 105 110 115
 Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
 120 125 130
 Asn Gln Gln Phe

<210> 97
 <211> 1855
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..504

<220>
 <221> 3'UTR
 <222> 505..1855

<220>
 <221> polyA_signal
 <222> 1819..1824

<220>
 <221> polyA_site
 <222> 1840..1855

<400> 97
 tccccgggccg ccgccgttgc gctcgccgcg ctcgcactga agccccgggcc ctgcgcgcgcc 60
 gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctg 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
 75 80 85
 tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
 90 95 100 105
 gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
 Ala
 cctcccaggc ccctggggca gccctccgc cgcaggtttc aggtcccagg cccagctga 614
 ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
 cgtgttcgcc atcactgcgg ccggcgccag ccacgcgcgc acgcaggcct gttctatggg 734
 cgagctgctg cagtgcggct gccaggcgcc ccgcggggcg gccccctccc ggccctccgg 794
 cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgcgcctg 854
 ggagtgggga ggctgcggcg acgacgtgga cttcgggggac gagaagtcga ggctctttat 914
 ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974

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cgagggcgggc aggctggccg tgcggagcca cacgcgcacc gagtgcaaat gccacgggct 1034
gtcgggatca tgcgcgctgc gcacctgctg gcagaagctg cctccatttc gcgaggtggg 1094
cgcgcggctg ctggagcgct tccacggcgc ctcacgcgtc atgggcacca acgacggcaa 1154
ggccctgctg cccgccgtcc gcacgtcaa gccgccgggc cgagcggacc tcctctacgc 1214
cgccgattcg cccgacttct gcgccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccgacct cagcggtctg gacctgctgt gctgcggccg 1334
cgggcaccgc caggagagcg tgcagctcga agagaactgc ctgtgccgct tccactggtg 1394
ctgcgtagta cagtgccacc gctgccgtgt gcgcaaggag ctcagcctct gcctgtgacc 1454
cgccgccccg cgcgtagact gacttcgcgc agcgggtggc cgcacctgtg ggacctcagg 1514
gcaccggcac cgggcgcctc tcgcccgtcg agcccagcct ctccctgcca aagcccaact 1574
cccagggctc tggaaatggg gaggcgaggg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agttttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaa tgctggccac aggatggtgg gtgagggttag 1814
tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

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<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
          -20          -15          -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
          -5          1          5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
  10          15          20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 25          30          35          40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
          45          50          55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
          60          65          70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
          75          80          85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
          90          95          100
Ala
105

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<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

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<220>
<221> CDS
<222> 95..613

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<220>
<221> 3'UTR
<222> 614..667

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<220>

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<221> polyA_signal
 <222> 636..641

<220>
 <221> polyA_site
 <222> 652..667

<400> 99
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 gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
 Met Ile Val Lys Gly Val Ala
 1 5
 tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
 Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
 10 15 20
 tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
 Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
 25 30 35
 gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
 Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
 40 45 50 55
 ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
 Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
 60 65 70
 acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
 Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
 75 80 85
 aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
 Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
 90 95 100
 gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
 Glu Glu Gly Lys Lys Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
 105 110 115
 tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
 Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
 120 125 130 135
 gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
 Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
 140 145 150
 gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
 Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
 155 160 165
 caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
 Gln Thr Thr Val Lys Asn
 170
 tctttcgcaa aaaaaaaaaa aaaa 667

<210> 100
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
 1 5 10 15
 Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
 20 25 30
 Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
 35 40 45
 Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
 50 55 60
 Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
 65 70 75 80

His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
 85 90 95
 Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
 100 105 110
 Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
 115 120 125
 Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
 130 135 140
 Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
 145 150 155 160
 Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
 165 170

<210> 101
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..153

<220>
 <221> CDS
 <222> 154..639

<220>
 <221> 3'UTR
 <222> 640..1062

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1047..1062

<400> 101
 attggtgtat ggctttgcag caataactga tggctgtttc ccctcctgct ttatctttca 60
 gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
 gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
 Met Ala Cys Trp Pro Gln Leu
 1 5
 agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
 Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
 10 15 20
 cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
 Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
 25 30 35
 atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
 Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
 40 45 50 55
 ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
 Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
 60 65 70
 ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
 Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
 75 80 85
 ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
 Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
 90 95 100
 cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac 510

<220>
 <221> polyA_site
 <222> 63..933

<400> 103
 aaaccctcag ggacctggtg tagacgcaga atctgtttca cacaacaact gctatttgaa 60
 ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
 cagatgtgta cggatgaaaa tacagttag atg agt cag aaa ccg gcc aag gag 173
 Met Ser Gln Lys Pro Ala Lys Glu
 1 5
 ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
 Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
 10 15 20
 cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
 His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
 25 30 35 40
 gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
 Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
 45 50 55
 gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
 Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
 60 65 70
 aag atc agg cca acc cca aag aag aag tgaccaagga ggagttttaa 412
 Lys Ile Arg Pro Thr Pro Lys Lys Lys
 75 80
 ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac ccctggatga 472
 agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
 gctcatggtc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
 tcatcccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
 atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
 tggaaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
 gcgtgggtggc gggcgccctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
 gaacctggga ggcggagctt gcagttagcc gagatcgcac cactgcactc cagcctgggc 892
 gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933

<210> 104
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
 1 5 10 15
 Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
 20 25 30
 Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
 35 40 45
 Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
 50 55 60
 Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
 65 70 75 80
 Lys

<210> 105
 <211> 1187
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..34


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Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu
  215                220                225
tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct      823
Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser
  230                235                240                245
tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga      871
Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg
                250                255                260
gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa      919
Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys
                265                270                275
gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag      967
Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu
                280                285                290
gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag      1015
Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys
                295                300                305
gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag      1063
Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys
  310                315                320                325
cca tgc taagggtggtt ttcagattcc acataaaaatg tcacacttgt ttcttgttca      1119
Pro Cys
tccaaggaac ctaattgaaa tttaaaaata aagctactga atttattgcc gcaaaaaaaaaa 1179
aaaaaaaaa      1187

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<210> 106
 <211> 345
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..19

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<400> 106
Met Ile Ser Pro Val Leu Ile Leu Phe Ser Ser Phe Leu Cys His Val
                -15                -10                -5
Ala Ile Ala Gly Arg Thr Cys Pro Lys Pro Asp Asp Leu Pro Phe Ser
                1                5                10
Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr
                15                20                25
Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe
  30                35                40                45
Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr
                50                55                60
Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg
                65                70                75
Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr
                80                85                90
Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly
                95                100                105
Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro
  110                115                120                125
Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala
                130                135                140
Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro
                145                150                155
Gln His Ala Met Phe Gly Asn Asp Thr Ile Thr Cys Thr Thr His Gly
                160                165                170
Asn Trp Thr Lys Leu Pro Glu Cys Arg Glu Val Lys Cys Pro Phe Pro
                175                180                185
Ser Arg Pro Asp Asn Gly Phe Val Asn Tyr Pro Ala Lys Pro Thr Leu
  190                195                200                205

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Tyr Tyr Lys Asp Lys Ala Thr Phe Gly Cys His Asp Gly Tyr Ser Leu
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 Asp Gly Pro Glu Glu Ile Glu Cys Thr Lys Leu Gly Asn Trp Ser Ala
 225 230 235
 Met Pro Ser Cys Lys Ala Ser Cys Lys Val Pro Val Lys Lys Ala Thr
 240 245 250
 Val Val Tyr Gln Gly Glu Arg Val Lys Ile Gln Glu Lys Phe Lys Asn
 255 260 265
 Gly Met Leu His Gly Asp Lys Val Ser Phe Phe Cys Lys Asn Lys Glu
 270 275 280 285
 Lys Lys Cys Ser Tyr Thr Glu Asp Ala Gln Cys Ile Asp Gly Thr Ile
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 Thr Asp Ala Ser Asp Val Lys Pro Cys
 320 325

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 Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr
 15 20 25
 tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag 147
 Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys
 30 35 40
 aag cgg ggc tgg cgg cgg ctt gct cag gag ccg ctg ggg ctg gag gtt 195
 Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val
 45 50 55 60
 gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc 243
 Asp Gln Phe Leu Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly
 65 70 75
 ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc 291
 Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly
 80 85 90
 tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag 339
 Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys

95	100	105	387
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac			
Ser Leu Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn			
110	115	120	
aca tcc aaa gtc cct gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc			435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro			
125	130	135	140
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc			
Asn Ala Lys Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala			483
145	150	155	
aag cag ggc gag ctg ccc cgg gag gtg cgc agg gcc cag gcc cgg ctc			531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu			
160	165	170	
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gac acc gta			579
Leu Asn Pro Ser Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val			
175	180	185	
gag cgg ccc ttc tac gac ctc tgg gcc tca gac aac ccc ctg gac agg			627
Glu Arg Pro Phe Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg			
190	195	200	
ccg ttg gtt ggc cag gat gag ttt ttc ctg gag cag acc aag aag aaa			675
Pro Leu Val Gly Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys			
205	210	215	220
gga gtg aag cgg cca gca cgc ctg cac acc aag ccg tcc cag gca ccc			723
Gly Val Lys Arg Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro			
225	230	235	
gcc gtg gag gtg gcg cct gcc gga gct tcc tac aat cca tcc ttt gaa			771
Ala Val Glu Val Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu			
240	245	250	
gac cac cag acc ctg ctc tca gcg gcc cac gag gtg gag ttg cag cgg			819
Asp His Gln Thr Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg			
255	260	265	
cag aag gag gcg gag aag ctg gag cgg cag ctg gcc ctg ccc gcc acg			867
Gln Lys Glu Ala Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr			
270	275	280	
gag cag gcc gcc acc cag gag tcc aca ttc cag gag ctg tgc gag ggg			915
Glu Gln Ala Ala Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly			
285	290	295	300
ctg ctg gag gag tcg gat ggt gag ggg gag cca ggc cag ggc gag ggg			963
Leu Leu Glu Glu Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly			
305	310	315	
ccg gag gct ggg gat gcc gag gtc tgt ccc acg ccc gcc cgc ctg gcc			1011
Pro Glu Ala Gly Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala			
320	325	330	
acc aca gag aag aag acg gag cag cag cgg cgg cgg gag aag gct gtg			1059
Thr Thr Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val			
335	340	345	
cac agg ctg cgg gta cag cag gcc gcg ttg cgg gcc gcc cgg ctc cgg			1107
His Arg Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg			
350	355	360	
cac cag gag ctg ttc cgg ctg cgc ggg atc aag gcc cag gtg gcc ctg			1155
His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu			
365	370	375	380
agg ctg gcg gag ctg gcg cgg cgg cag agg cgg cgg cag gcg cgg cgg			1203
Arg Leu Ala Glu Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg			
385	390	395	
gag gct gag gct gac aag ccc cga agg ctg ggg cgg ctc aag tac cag			1251
Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln			
400	405	410	
gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc			1299
Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu			
415	420	425	
agg acc ctg aag ccc gag ggc aac atc ctt cga gac cgg ttc aag agc			1347
Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser			

Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
370 375 380
Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala
385 390 395 400
Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
405 410 415
Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
420 425 430
Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
435 440 445
Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
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Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
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<213> Homo sapiens

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<222> 1253..1789

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<220>
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<222> 1774..1789

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tctgccaagc ttctccgata cccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115
Met Cys Leu Leu Leu Ser Cys
-10
cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr
-5 1 5
tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
10 15 20 25
gtg gtg cac atg tcg cag acc aca att agt cct ctg gag aat gcc ata 259
Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile
30 35 40
gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307
Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln
45 50 55
tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355
Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu
60 65 70
aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag 403
Asn Gly Ile Val Asp Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu
75 80 85

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aag gcc ttc ttc act gaa gag tat gtc agg gac cac cct gag gac cag 451
Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg Asp His Pro Glu Asp Gln
90 95 100 105
gac aag ctg acc cac ctc aag gac ctg att gca tgg cag atc ccc ttc 499
Asp Lys Leu Thr His Leu Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe
110 115 120
ttg gga gct ggg att aag atc cat gag aaa agg gtg tca gat aac ttg 547
Leu Gly Ala Gly Ile Lys Ile His Glu Lys Arg Val Ser Asp Asn Leu
125 130 135
cga ccc ttc cat gac cgg atg gag gaa tgt ttc aag aac ctg aaa atg 595
Arg Pro Phe His Asp Arg Met Glu Glu Cys Phe Lys Asn Leu Lys Met
140 145 150
aag gtg gag aag gag tac ggt gtc cga gag atg cct gac ttt gac gac 643
Lys Val Glu Lys Glu Tyr Gly Val Arg Glu Met Pro Asp Phe Asp Asp
155 160 165
agg aga gtg ggc cgt ccc agg tct atg ctg cgc tca tac aga cag atg 691
Arg Arg Val Gly Arg Pro Arg Ser Met Leu Arg Ser Tyr Arg Gln Met
170 175 180 185
tcc atc atc tct ctg gct tcc atg aat tct gac tgc agc acc ccc agc 739
Ser Ile Ile Ser Leu Ala Ser Met Asn Ser Asp Cys Ser Thr Pro Ser
190 195 200
aag cct acc tca gag agc ttt gac ctg gaa tta gca tca ccc aag acg 787
Lys Pro Thr Ser Glu Ser Phe Asp Leu Glu Leu Ala Ser Pro Lys Thr
205 210 215
ccg aga gtg gag cag gag gaa ccg atc tcc ccg ggg agc acc ctg cct 835
Pro Arg Val Glu Gln Glu Glu Pro Ile Ser Pro Gly Ser Thr Leu Pro
220 225 230
gag gtc aag ctg cgg agg tcc aag aag agg aca aag aga agc agc gta 883
Glu Val Lys Leu Arg Arg Ser Lys Lys Arg Thr Lys Arg Ser Ser Val
235 240 245
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Val Phe Ala Asp Glu Lys Ala Ala Ala Glu Ser Asp Leu Lys Arg Leu
250 255 260 265
tcc agg aag cat gag ttc atg agt gac acc aac ctc tcg gag cat gcg 979
Ser Arg Lys His Glu Phe Met Ser Asp Thr Asn Leu Ser Glu His Ala
270 275 280
gcc atc ccc ctc aag gcg tct gtc ctc tct caa atg agc ttt gcc agc 1027
Ala Ile Pro Leu Lys Ala Ser Val Leu Ser Gln Met Ser Phe Ala Ser
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Gln Ser Met Pro Thr Ile Pro Ala Leu Ala Leu Ser Val Ala Gly Ile
300 305 310
cct ggg ttg gat gag gcc aac aca tct ccc cgc ctc agc cag acc ttc 1123
Pro Gly Leu Asp Glu Ala Asn Thr Ser Pro Arg Leu Ser Gln Thr Phe
315 320 325
ctc caa ctc tca gat ggt gac aag aag aca ctc aca cgg aag aag gtc 1171
Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val
330 335 340 345
aat cag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc 1219
Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly
350 355 360
aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg 1272
Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu
365 370
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aagcctcaga gagtgggaga ctgtcccat cagttgtcct tacttagagg agacagagag 1392
gccaatcagg tcccagagct tgaatgctaa caagcccagc atcccctggg gctgtgatca 1452
tggtggatga ggaagcctca acgtagattc ctgaactcaa ggtaccagca agaatgcctt 1512
ctcccagtg gctctcccca acatcctagg cacagctttc ataaccagcgt ttcttaggtg 1572
taagaaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632
taaataattct ttttaatttt atttttagatt aacagttttg tactttacat ttttttatac 1692
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 <212> PRT
 <213> Homo sapiens

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 Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
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 Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
 35 40 45
 Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
 50 55 60 65
 Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
 70 75 80
 Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
 85 90 95
 Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
 100 105 110
 Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
 115 120 125
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
 130 135 140 145
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
 150 155 160
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
 165 170 175
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
 180 185 190
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
 195 200 205
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
 210 215 220 225
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
 230 235 240
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
 245 250 255
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
 260 265 270
 Thr Asn Leu Ser Glu His Ala Ile Pro Leu Lys Ala Ser Val Leu
 275 280 285
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
 290 295 300 305
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
 310 315 320
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
 325 330 335
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
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 Asp Leu
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<220>
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 <222> 1365..1408

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 Met Ser Thr Phe
 1
 ttc tgc gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
 Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
 5 10 15 20
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 Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
 25 30 35
 tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
 Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
 40 45 50
 tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
 Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
 55 60 65
 tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
 Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
 70 75 80
 gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
 Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
 85 90 95 100
 tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
 Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu
 105 110 115
 aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498
 Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
 120 125 130
 tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
 Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
 135 140 145
 tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
 Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
 150 155 160
 atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642
 Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
 165 170 175 180
 ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690


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185 190 195
gtg gag gtc aca aag acg ttt ttg cct ctt aga aaa tcc aaa ggg 738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly
200 205 210
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg 786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg
215 220 225
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca 834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser
230 235 240
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc 882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile
245 250 255 260
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg 930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp
265 270 275
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag 978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln
280 285 290
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta 1026
Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu
295 300 305
ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac 1074
Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp
310 315 320
atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca 1122
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro
325 330 335 340
ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att 1170
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile
345 350 355
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc 1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro
360 365 370
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc 1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro
375 380 385
taggcaatgg aagccctcaa agaagtcgga atgtcatagt cttgaaatga aagggaaact 1323
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<210> 112
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
 50 55 60
 Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val
 65 70 75 80
 Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His
 85 90 95
 Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly
 100 105 110
 Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys

